



# SEQUENCE LISTING

<110> YOSHINAGA, STEVEN KIYOSHI

<120> POLYPEPTIDES INVOLVED IN IMMUNE RESPONSE

<130> A-579B

<140> US 09/890,729

<141> 2001-08-03

<150> PCT US00/01871

<151> 2000-01-27

<150> 09/264,527

<151> 1999-03-08

<150> 09/244,448

<151> 1999-02-03

<160> 37

<170> PatentIn version 3.2

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<212> DNA

<213> Mus musculus

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<221> CDS

<222> (1)..(600)

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Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg	
1 5 10 15	

ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca	96
Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser	
20 25 30	

ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc	144
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val	
35 40 45	

cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa	192
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu	
50 55 60	

ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca	240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro	
65 70 75 80	

atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta	288
Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	
85 90 95	

aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc	336
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser	
100 105 110	

att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat	384
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Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr		
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ttg	cat	att	tat	gaa	tcc	cag	ctc	tgc	tgc	cag	ctg	aag	ctc	tgg	cta		432
Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu		
		130				135					140						
ccc	gta	ggg	tgt	gca	gct	ttc	gtt	gtg	gta	ctc	ctt	ttt	gga	tgc	ata		480
Pro	Val	Gly	Cys	Ala	Ala	Phe	Val	Val	Val	Leu	Leu	Phe	Gly	Cys	Ile		
		145			150					155					160		
ctt	atc	atc	tgg	ttt	tca	aaa	aag	aaa	tac	gga	tcc	agt	gtg	cat	gac		528
Leu	Ile	Ile	Trp	Phe	Ser	Lys	Lys	Lys	Tyr	Gly	Ser	Ser	Val	His	Asp		
				165					170					175			
cct	aat	agt	gaa	tac	atg	ttc	atg	gcg	gca	gtc	aac	aca	aac	aaa	aag		576
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys		
			180					185					190				
tct	aga	ctt	gca	ggt	gtg	acc	tca										600
Ser	Arg	Leu	Ala	Gly	Val	Thr	Ser										
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			20					25					30				
Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val		
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Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu		
		50				55					60						
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Ala	Val	Ser	Ile	Lys	Asn	Pro		
65					70					75					80		
Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu		
				85					90					95			
Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser		
			100					105					110				
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr		
		115					120					125					
Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu		

130                                      135                                      140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
145                                      150                                      155                                      160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp  
                                    165                                      170                                      175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
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Ser Arg Leu Ala Gly Val Thr Ser  
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Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser  
                                    20                                      25                                      30

Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val  
                                    35                                      40                                      45

Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu  
50                                      55                                      60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro  
65                                      70                                      75

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
                                    85                                      90                                      95

Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser  
                                    100                                      105                                      110

Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr  
115                                      120                                      125

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
130                                      135                                      140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
145                                      150                                      155                                      160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp  
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser  
195 200

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Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val  
20 25 30

Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu  
35 40 45

Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val  
50 55 60

Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg  
65 70 75 80

Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val  
85 90 95

Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe  
100 105 110

Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg  
115 120 125

Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr  
130 135 140

Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val  
145 150 155 160

Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp  
165 170 175

Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met  
180 185 190

Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala  
195 200 205

Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro  
210 215

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Asn Tyr Phe Cys Pro Pro Pro Ser Gly His Ile Glu Leu Cys Lys Leu  
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Trp Leu Val Phe Leu Leu Leu Ile Trp Pro Arg Ala  
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<220>  
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Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro  
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ggt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt 96  
Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly  
20 25 30  
  
ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act 144  
Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr  
35 40 45  
  
gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac 192  
Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp  
50 55 60  
  
ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa 240  
Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln

65	70	75	80	
atc gaa aac cca gaa gtt tgc gtg act tac tac ctg cct tac aag tct	Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser	85 90	95	288
cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc	Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser	100 105	110	336
ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc	Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val	115 120	125	384
acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca	Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr	130 135	140	432
gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg	Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val	145 150	155	480
gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac	Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn	165 170	175	528
ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca	Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro	180 185	190	576
gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac	Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp	195 200	205	624
acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat	Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr	210 215	220	672
gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt	Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val	225 230	235	720
ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att	Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile	245 250	255	768
agc cag gca gaa agt ttc act gga aat aac aca aag aac cca cag gaa	Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu	260 265	270	816
acc cac aat aat gag tta aaa gtc ctt gtc ccc gtc ctt gct gta ctg	Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu	275 280	285	864
gcg gca gcg gca ttc gtt tcc ttc atc ata tac aga cgc acg cgt ccc	Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro	290 295	300	912
cac cga agc tat aca gga ccc aag act gta cag ctt gaa ctt aca gac	His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp	305 310	315	960
cac gcc	His Ala			966

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Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro  
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Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly  
20 25 30

Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr  
35 40 45

Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp  
50 55 60

Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln  
65 70 75 80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser  
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser  
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val  
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr  
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val  
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn  
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro  
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp  
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr  
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val  
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile  
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu  
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu  
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro  
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp  
305 310 315 320

His Ala

<210> 8  
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<213> Mus musculus

<400> 8

Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro  
1 5 10 15

Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly  
20 25 30

Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr  
35 40 45

Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp  
50 55 60

Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln  
65 70 75 80

Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser  
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser  
100 105 110



Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val  
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr  
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val  
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn  
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro  
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp  
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr  
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val  
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile  
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu  
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu  
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro  
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp  
305 310 315 320

His Ala

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<212> PRT  
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<400> 9

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20 25 30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp  
35 40 45

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser  
50 55 60

Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val  
65 70 75 80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu  
85 90 95

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser  
100 105 110

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr  
115 120 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp  
130 135 140

Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr  
145 150 155 160

Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe  
165 170 175

Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile  
180 185 190

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp  
195 200 205

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly  
210 215 220

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp  
225 230 235 240

Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly  
245 250 255

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys  
260 265 270

Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn  
275 280 285

Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val  
290 295 300

Phe Leu  
305

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<212> PRT  
<213> Artificial sequence

<220>  
<223> Synthetic

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Met Cys Cys Leu Pro Leu Leu Leu Phe Leu Leu Ser Val Val Leu Cys  
1 5 10 15

His Ser Tyr Trp Gln Val Leu Val Tyr Lys Asn Arg Leu Ser Leu Asp  
20 25 30

Cys Val Val Leu Ala Phe Ser Thr Pro Ile Ser Arg Thr Cys Gly Pro  
35 40 45

Pro Trp Asn Ile Thr Thr Val Asn Val Val Val Phe Arg Ser Thr Gly  
50 55 60

Pro Glu Thr  
65

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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(864)

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Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu  
1 5 10 15

cga gct gat act cag gag aag gaa gtc aga gcg atg gta ggc agc gac 96  
Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp  
20 25 30

gtg	gag	ctc	agc	tgc	gct	tgc	cct	gaa	gga	agc	cgt	ttt	gat	tta	aat	144
Val	Glu	Leu	Ser	Cys	Ala	Cys	Pro	Glu	Gly	Ser	Arg	Phe	Asp	Leu	Asn	
	35						40					45				
gat	gtt	tac	gta	tat	tgg	caa	acc	agt	gag	tcg	aaa	acc	gtg	gtg	acc	192
Asp	Val	Tyr	Val	Tyr	Trp	Gln	Thr	Ser	Glu	Ser	Lys	Thr	Val	Val	Thr	
	50					55					60					
tac	cac	atc	cca	cag	aac	agc	tcc	ttg	gaa	aac	gtg	gac	agc	cgc	tac	240
Tyr	His	Ile	Pro	Gln	Asn	Ser	Ser	Leu	Glu	Asn	Val	Asp	Ser	Arg	Tyr	
65					70					75					80	
cgg	aac	cga	gcc	ctg	atg	tca	ccg	gcc	ggc	atg	ctg	cgg	ggc	gac	ttc	288
Arg	Asn	Arg	Ala	Leu	Met	Ser	Pro	Ala	Gly	Met	Leu	Arg	Gly	Asp	Phe	
				85					90					95		
tcc	ctg	cgc	ttg	ttc	aac	gtc	acc	ccc	cag	gac	gag	cag	aag	ttt	cac	336
Ser	Leu	Arg	Leu	Phe	Asn	Val	Thr	Pro	Gln	Asp	Glu	Gln	Lys	Phe	His	
			100					105					110			
tgc	ctg	gtg	ttg	agc	caa	tcc	ctg	gga	ttc	cag	gag	gtt	ttg	agc	gtt	384
Cys	Leu	Val	Leu	Ser	Gln	Ser	Leu	Gly	Phe	Gln	Glu	Val	Leu	Ser	Val	
		115					120					125				
gag	gtt	aca	ctg	cat	gtg	gca	gca	aac	ttc	agc	gtg	ccc	gtc	gtc	agc	432
Glu	Val	Thr	Leu	His	Val	Ala	Ala	Asn	Phe	Ser	Val	Pro	Val	Val	Ser	
	130					135					140					
gcc	ccc	cac	agc	ccc	tcc	cag	gat	gag	ctc	acc	ttc	acg	tgt	aca	tcc	480
Ala	Pro	His	Ser	Pro	Ser	Gln	Asp	Glu	Leu	Thr	Phe	Thr	Cys	Thr	Ser	
145					150					155					160	
ata	aac	ggc	tac	ccc	agg	ccc	aac	gtg	tac	tgg	atc	aat	aag	acg	gac	528
Ile	Asn	Gly	Tyr	Pro	Arg	Pro	Asn	Val	Tyr	Trp	Ile	Asn	Lys	Thr	Asp	
				165					170				175			
aac	agc	ctg	ctg	gac	cag	gct	ctg	cag	aat	gac	acc	gtc	ttc	ttg	aac	576
Asn	Ser	Leu	Leu	Asp	Gln	Ala	Leu	Gln	Asn	Asp	Thr	Val	Phe	Leu	Asn	
			180					185					190			
atg	cgg	ggc	ttg	tat	gac	gtg	gtc	agc	gtg	ctg	agg	atc	gca	cgg	acc	624
Met	Arg	Gly	Leu	Tyr	Asp	Val	Val	Ser	Val	Leu	Arg	Ile	Ala	Arg	Thr	
		195					200					205				
ccc	agc	gtg	aac	att	ggc	tgc	tgc	ata	gag	aac	gtg	ctt	ctg	cag	cag	672
Pro	Ser	Val	Asn	Ile	Gly	Cys	Cys	Ile	Glu	Asn	Val	Leu	Leu	Gln	Gln	
	210					215					220					
aac	ctg	act	gtc	ggc	agc	cag	aca	gga	aat	gac	atc	gga	gag	aga	gac	720
Asn	Leu	Thr	Val	Gly	Ser	Gln	Thr	Gly	Asn	Asp	Ile	Gly	Glu	Arg	Asp	
225					230					235					240	
aag	atc	aca	gag	aat	cca	gtc	agt	acc	ggc	gag	aaa	aac	gcg	gcc	acg	768
Lys	Ile	Thr	Glu	Asn	Pro	Val	Ser	Thr	Gly	Glu	Lys	Asn	Ala	Ala	Thr	
				245					250					255		
tgg	agc	atc	ctg	gct	gtc	ctg	tgc	ctg	ctt	gtg	gtc	gtg	gcg	gtg	gcc	816
Trp	Ser	Ile	Leu	Ala	Val	Leu	Cys	Leu	Leu	Val	Val	Val	Ala	Val	Ala	
			260				265						270			
ata	ggc	tgg	gtg	tgc	agg	gac	cga	tgc	ctc	caa	cac	agc	tat	gca	ggc	864
Ile	Gly	Trp	Val	Cys	Arg	Asp	Arg	Cys	Leu	Gln	His	Ser	Tyr	Ala	Gly	
		275					280					285				

<210> 12  
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<212> PRT  
<213> Homo sapiens

<400> 12

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu  
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp  
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn  
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr  
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr  
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe  
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His  
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val  
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser  
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser  
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp  
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn  
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr  
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln  
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp  
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr  
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala  
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly  
275 280 285

<210> 13  
<211> 267  
<212> PRT  
<213> Homo sapiens

<400> 13

Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp Val Glu Leu Ser Cys  
1 5 10 15

Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn Asp Val Tyr Val Tyr  
20 25 30

Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr Tyr His Ile Pro Gln  
35 40 45

Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu  
50 55 60

Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe Ser Leu Arg Leu Phe  
65 70 75 80

Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His Cys Leu Val Leu Ser  
85 90 95

Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu Val Thr Leu His  
100 105 110

Val Ala Ala Asn Phe Ser Val Pro Val Val Ser Ala Pro His Ser Pro  
115 120 125

Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser Ile Asn Gly Tyr Pro  
130 135 140

Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp Asn Ser Leu Leu Asp  
145 150 155 160

Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn Met Arg Gly Leu Tyr  
165 170 175

Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr Pro Ser Val Asn Ile  
180 185 190

Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln Asn Leu Thr Val Gly  
195 200 205

Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp Lys Ile Thr Glu Asn  
210 215 220

Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr Trp Ser Ile Leu Ala  
225 230 235 240

Val Leu Cys Leu Leu Val Val Val Ala Val Ala Ile Gly Trp Val Cys  
245 250 255

Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly  
260 265

<210> 14  
<211> 276  
<212> PRT  
<213> Mus musculus

<400> 14

Glu Thr Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys  
1 5 10 15

Ile Asp Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr  
20 25 30

Trp Gln Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr  
35 40 45

Lys Ser Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His  
50 55 60

Leu Ser Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys  
65 70 75 80

Asn Val Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met  
85 90 95

Asn Thr Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu  
100 105 110

Arg Val Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser

115		120		125
Ser Asn Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly				
130		135		140
Tyr Pro Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu				
145		150		155
Ile Asp Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly				
	165		170	175
Leu Tyr Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly				
	180		185	190
Asp Val Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr				
	195		200	205
Ser Ile Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro				
210		215		220
Gln Glu Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala				
225		230		235
Val Leu Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr				
	245		250	255
Arg Pro His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu				
	260		265	270
Thr Asp His Ala				
	275			

<210> 15  
 <211> 125  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Synthetic

<400> 15

Glu Glu Val Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr
1 5 10 15
Val Tyr Trp Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg
20 25 30
Ser Met Gly Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys
35 40 45



Val Leu Val Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr  
50 55 60

Thr Cys Ser Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn  
65 70 75 80

Ser Leu Asp Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val  
85 90 95

Ser Leu Arg Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly  
100 105 110

Lys Lys Leu Ala Val Leu Val Ile Arg Arg Ser Tyr Gly  
115 120 125

<210> 16  
<211> 1294  
<212> DNA  
<213> Homo sapiens

<220>  
<221> 5'UTR  
<222> (1)..(199)

<220>  
<221> CDS  
<222> (200)..(1105)

<400> 16  
gctggtacgc ctgcaggtac cggctcggaa ttcccgggtc gacccacgcg tccgcccacg 60  
cgctcgcggg agcgcagtta gagccgatct cccgcgcccc gaggttgctc ctctccgagg 120  
tctcccgcgg cccaagttct ccgcgccccg aggtctccgc gccccgaggt ctccgcggcc 180  
cgaggtctcc gcccgacc atg cgg ctg ggc agt cct gga ctg ctc ttc ctg 232  
Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu  
1 5 10  
ctc ttc agc agc ctt cga gct gat act cag gag aag gaa gtc aga gcg 280  
Leu Phe Ser Ser Leu Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala  
15 20 25  
atg gta ggc agc gac gtg gag ctc agc tgc gct tgc cct gaa gga agc 328  
Met Val Gly Ser Asp Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser  
30 35 40  
cgt ttt gat tta aat gat gtt tac gta tat tgg caa acc agt gag tcg 376  
Arg Phe Asp Leu Asn Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser  
45 50 55  
aaa acc gtg gtg acc tac cac atc cca cag aac agc tcc ttg gaa aac 424  
Lys Thr Val Val Thr Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn  
60 65 70 75  
gtg gac agc cgc tac cgg aac cga gcc ctg atg tca ccg gcc ggc atg 472  
Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met



<210> 17  
<211> 302  
<212> PRT  
<213> Homo sapiens

<400> 17

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu  
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp  
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn  
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr  
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr  
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe  
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His  
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val  
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser  
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser  
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp  
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn  
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr  
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln  
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp  
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr  
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala  
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly  
275 280 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val  
290 295 300

<210> 18  
<211> 302  
<212> PRT  
<213> Homo sapiens

<400> 18

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu  
1 5 10 15

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp  
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn  
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr  
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr  
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe  
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His  
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val  
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser  
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser



Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser  
85 90 95

Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser  
100 105 110

Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val  
115 120 125

Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr  
130 135 140

Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val  
145 150 155 160

Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn  
165 170 175

Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro  
180 185 190

Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp  
195 200 205

Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr  
210 215 220

Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val  
225 230 235 240

Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile  
245 250 255

Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu  
260 265 270

Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu  
275 280 285

Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro  
290 295 300

His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp  
305 310 315 320

His Ala

<210> 20  
 <211> 143  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Synthetic

<400> 20

Met Leu Pro Gly Leu Leu Phe Leu Leu Ser Ser Leu Ala Glu Glu Val  
 1 5 10 15

Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr Val Tyr Trp  
 20 25 30

Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg Ser Met Gly  
 35 40 45

Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys Val Leu Val  
 50 55 60

Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr Thr Cys Ser  
 65 70 75 80

Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn Ser Leu Asp  
 85 90 95

Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val Ser Leu Arg  
 100 105 110

Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly Lys Lys Leu  
 115 120 125

Ala Val Leu Val Ile Arg Arg Ser Tyr Gly Val Glu Leu Thr His  
 130 135 140

<210> 21  
 <211> 1370  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> 5'UTR  
 <222> (1)..(165)

<220>  
 <221> CDS  
 <222> (166)..(762)

<400> 21  
 aacaatttca cacaggaaac agctatgacc atgattacgc caagctctaa tacgactcac 60

tatagggaaa gctggtacgc ctgcaggtac cggtcgga tccccgggtc gacccacgcg	120
tccgtgaaca ctgaacgcga ggactgttaa ctgtttctgg caaac atg aag tca ggc	177
Met Lys Ser Gly	
1	
ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa gtt tta aca gga	225
Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly	
5 10 15 20	
gaa atc aat ggt tct gcc aat tat gag atg ttt ata ttt cac aac gga	273
Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly	
25 30 35	
ggt gta caa att tta tgc aaa tat cct gac att gtc cag caa ttt aaa	321
Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys	
40 45 50	
atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat ctc act aag aca	369
Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr	
55 60 65	
aaa gga agt gga aac aca gtg tcc att aag agt ctg aaa ttc tgc cat	417
Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His	
70 75 80	
tct cag tta tcc aac aac agt gtc tct ttt ttt cta tac aac ttg gac	465
Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp	
85 90 95 100	
cat tct cat gcc aac tat tac ttc tgc aac cta tca att ttt gat cct	513
His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro	
105 110 115	
cct cct ttt aaa gta act ctt aca gga gga tat ttg cat att tat gaa	561
Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu	
120 125 130	
tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc ata gga tgt gca	609
Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro Ile Gly Cys Ala	
135 140 145	
gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt att tgt tgg ctt	657
Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu	
150 155 160	
aca aaa aag aag tat tca tcc agt gtg cac gac cct aac ggt gaa tac	705
Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr	
165 170 175 180	
atg ttc atg aga gca gtg aac aca gcc aaa aaa tct aga ctc aca gat	753
Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp	
185 190 195	
gtg acc cta taatatggaa ctctggcacc caggcatgaa gcacgttggc	802
Val Thr Leu	
cagtttttcc caacttgaag tgcaagattc tcttatttcc gggaccacgg agagtctgac	862
ttactacat acatcttctg ctgggtgtttt gttcaatctg gaagaatgac tgtatcagtc	922
aatggggatt ttaacagact gccttggtac tgccgagtc tctcaaaaca aacaccctct	982



tgcaaccagc tttggagaaa gccagctcc tgtgtgctca ctgggagtgg aatccctgtc 1042  
 tccacatctg ctctagcag tgcacagcc agtaaaacaa acacatttac aagaaaaatg 1102  
 ttttaaagat gccaggggta ctgaatctgc aaagcaaag agcagccaag gaccagcatc 1162  
 tgtccgcatt tcactatcat actacctctt ctttctgtag ggatgagaat tcctctttta 1222  
 atcagtcaag ggagatgctt caaagctgga gctattttat ttctgagatg ttgatgtgaa 1282  
 ctgtacatta gtacatactc agtactctcc ttcaattgct gaaccccagt tgaccatttt 1342  
 accaagactt tagatgcttt cttgtgcc 1370

<210> 22  
 <211> 199  
 <212> PRT  
 <213> Homo sapiens

<400> 22

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys  
 1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile  
 20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val  
 35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp  
 50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu  
 65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
 85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser  
 100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu  
 115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro  
 130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu  
 145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro

	165		170		175
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser	180		185		190
Arg Leu Thr Asp Val Thr Leu	195				
<210> 23					
<211> 199					
<212> PRT					
<213> Homo sapiens					
<400> 23					
Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys	1	5	10		15
Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile	20		25		30
Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val	35		40		45
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp	50		55		60
Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu	65		70		75
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	85		90		95
Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser	100		105		110
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu	115		120		125
His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro	130		135		140
Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu	145		150		155
Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro	165		170		175
Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser	180		185		190

Arg Leu Thr Asp Val Thr Leu  
195

<210> 24  
<211> 200  
<212> PRT  
<213> Mus musculus

<400> 24

Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg  
1 5 10 15

Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser  
20 25 30

Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val  
35 40 45

Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu  
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro  
65 70 75 80

Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
85 90 95

Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser  
100 105 110

Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr  
115 120 125

Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
130 135 140

Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
145 150 155 160

Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp  
165 170 175

Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
180 185 190

Ser Arg Leu Ala Gly Val Thr Ser  
195 200

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> Synthetic oglionucleotide  
  
<400> 25  
accatgcggc tgggcagtc tggga 24  
  
<210> 26  
<211> 23  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> Synthetic oglionucleotide  
  
<400> 26  
tggtgacctt ccacatccca cag 23  
  
<210> 27  
<211> 23  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> Synthetic oglionucleotide  
  
<400> 27  
tccgatgtca tttcctgtct ggc 23  
  
<210> 28  
<211> 24  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> Synthetic oglionucleotide  
  
<400> 28  
gctctgtctc cggactcaca gccc 24  
  
<210> 29  
<211> 28  
<212> DNA  
<213> Artificial sequence  
  
<220>  
<223> Synthetic oglionucleotide  
  
<400> 29  
gtggcagcaa acttcagcgt gcccgctcg 28  
  
<210> 30  
<211> 28  
<212> DNA

<213> Artificial sequence  
<220>  
<223> Synthetic oglionucleotide  
<400> 30  
cccaacgtgt actggatcaa taagacgg 28  
  
<210> 31  
<211> 28  
<212> DNA  
<213> Artificial sequence  
<220>  
<223> Synthetic oglionucleotide  
<400> 31  
gcgtgctgag gatcgacgg acccccag 28  
  
<210> 32  
<211> 21  
<212> DNA  
<213> Artificial sequence  
<220>  
<223> Synthetic oglionucleotide  
<400> 32  
gcctctagaa agagctggga c 21  
  
<210> 33  
<211> 21  
<212> DNA  
<213> Artificial sequence  
<220>  
<223> Synthetic oglionucleotide  
<400> 33  
cgccgtgttc catttatgag c 21  
  
<210> 34  
<211> 18  
<212> DNA  
<213> Artificial sequence  
<220>  
<223> Synthetic oglionucleotide  
<400> 34  
gcatatttat gaatccca 18  
  
<210> 35  
<211> 18  
<212> DNA  
<213> Artificial sequence  
<220>  
<223> Synthetic oglionucleotide

<400> 35  
actattaggg tcatgcac

18

<210> 36  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Motif

<400> 36

Phe Asp Pro Pro Pro Phe  
1 5

<210> 37  
<211> 6  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Motif

<400> 37

Met Tyr Pro Pro Pro Tyr  
1 5